



SEQUENCE LISTING

<110> SCHLEHUBER, STEFFEN

<120> MUTEINS OF THE BILIN-BINDING PROTEIN

<130> 029029/0101

<140> 09/980,862

<141> 2001-12-07

<150> DE 199 26 068.0

<151> 1999-06-08

<160> 27

<170> PatentIn Ver. 2.1

<210> 1

<211> 1219

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: pBBP20
nucleic acid sequence

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<221> sig_peptide

<222> (22)..(84)

<220>

<221> mat_peptide

<222> (85)..(1209)

<223> fusion protein of bilin-binding protein, Strep-tag II
and fragment of phage coat protein pIII

<220>

<221> CDS

<222> (85)..(606)

<223> mature bilin-binding protein

<220>

<221> CDS

<222> (607)..(636)

<223> Strep-tag II-affinity tag

<220>

<221> misc_feature

<222> (637)..(639)

<223> amber stop codon

<220>

<221> CDS

<222> (640)..(1209)

<223> amino acids 217-406 of coat protein pIII

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Met Lys Lys Thr Ala Ile Ala Ile Ala Val
-20 -15

gca ctg gct ggt ttc gct acc gta gcg cag gcc gac gtg tac cac gac 99
Ala Leu Ala Gly Phe Ala Thr Val Ala Gln Ala Asp Val Tyr His Asp
-10 -5 -1 1 5

ggt gcc tgt ccc gaa gtc aag cca gtc gac aac ttc gac tgg tcc cag 147
Gly Ala Cys Pro Glu Val Lys Pro Val Asp Asn Phe Asp Trp Ser Gln
10 15 20

tac cat ggt aaa tgg tgg gaa gtc gcc aaa tac ccc aac tca gtt gag 195
Tyr His Gly Lys Trp Trp Glu Val Ala Lys Tyr Pro Asn Ser Val Glu
25 30 35

aag tac gga aag tgc gga tgg gct gag tac act cct gaa ggc aag agt 243
Lys Tyr Gly Lys Cys Gly Trp Ala Glu Tyr Thr Pro Glu Gly Lys Ser
40 45 50

gtc aaa gtt tcg aac tac cac gta atc cac ggc aag gaa tac ttt att 291
Val Lys Val Ser Asn Tyr His Val Ile His Gly Lys Glu Tyr Phe Ile
55 60 65

gaa gga act gcc tac cca gtt ggt gac tcc aag att gga aag atc tac 339
Glu Gly Thr Ala Tyr Pro Val Gly Asp Ser Lys Ile Gly Lys Ile Tyr
70 75 80 85

cac agc ctg act tac gga ggt gtc acc aag gag aac gta ttc aac gta 387
His Ser Leu Thr Tyr Gly Gly Val Thr Lys Glu Asn Val Phe Asn Val
90 95 100

ctc tcc act gac aac aag aac tac atc atc gga tac tac tgc aaa tac 435
Leu Ser Thr Asp Asn Lys Asn Tyr Ile Ile Gly Tyr Tyr Cys Lys Tyr
105 110 115

gac gag gac aag aag gga cac caa gac ttc gtc tgg gtg ctc tcc aga 483
Asp Glu Asp Lys Lys Gly His Gln Asp Phe Val Trp Val Leu Ser Arg
120 125 130

agc atg gtc ctt act ggt gaa gcc aag acc gct gtc gag aac tac ctt 531
Ser Met Val Leu Thr Gly Glu Ala Lys Thr Ala Val Glu Asn Tyr Leu
135 140 145

atc ggc tcc cca gta gtc gac tcc cag aaa ctg gta tac agt gac ttc 579
Ile Gly Ser Pro Val Val Asp Ser Gln Lys Leu Val Tyr Ser Asp Phe
150 155 160 165

tct gaa gcc gcc tgc aag gtc aac aat agc aac tgg tct cac ccg cag 627
Ser Glu Ala Ala Cys Lys Val Asn Asn Ser Asn Trp Ser His Pro Gln
170 175 180

ttc gaa aaa tag gct ggc ggc ggc tct ggt ggt ggt tct ggc ggc ggc 675
Phe Glu Lys Gln Ala Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly
185 190 195

tct gag ggt ggt ggc tct gag ggt ggc ggt tct gag ggt ggc ggc tct	723
Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser	
200 205 210	
gag gga ggc ggt tcc ggt ggt ggc tct ggt tcc ggt gat ttt gat tat	771
Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Ser Gly Asp Phe Asp Tyr	
215 220 225	
gaa aag atg gca aac gct aat aag ggg gct atg acc gaa aat gcc gat	819
Glu Lys Met Ala Asn Ala Asn Lys Gly Ala Met Thr Glu Asn Ala Asp	
230 235 240 245	
gaa aac gcg cta cag tct gac gct aaa ggc aaa ctt gat tct gtc gct	867
Glu Asn Ala Leu Gln Ser Asp Ala Lys Gly Lys Leu Asp Ser Val Ala	
250 255 260	
act gat tac ggt gct gct atc gat ggt ttc att ggt gac gtt tcc ggc	915
Thr Asp Tyr Gly Ala Ala Ile Asp Gly Phe Ile Gly Asp Val Ser Gly	
265 270 275	
ctt gct aat ggt aat ggt gct act ggt gat ttt gct ggc tct aat tcc	963
Leu Ala Asn Gly Asn Gly Ala Thr Gly Asp Phe Ala Gly Ser Asn Ser	
280 285 290	
caa atg gct caa gtc ggt gac ggt gat aat tca cct tta atg aat aat	1011
Gln Met Ala Gln Val Gly Asp Gly Asp Asn Ser Pro Leu Met Asn Asn	
295 300 305	
ttc cgt caa tat tta cct tcc ctc cct caa tcg gtt gaa tgt cgc cct	1059
Phe Arg Gln Tyr Leu Pro Ser Leu Pro Gln Ser Val Glu Cys Arg Pro	
310 315 320 325	
ttt gtc ttt ggc gct ggt aaa cca tat gaa ttt tct att gat tgt gac	1107
Phe Val Phe Gly Ala Gly Lys Pro Tyr Glu Phe Ser Ile Asp Cys Asp	
330 335 340	
aaa ata aac tta ttc cgt ggt gtc ttt gcg ttt ctt tta tat gtt gcc	1155
Lys Ile Asn Leu Phe Arg Gly Val Phe Ala Phe Leu Leu Tyr Val Ala	
345 350 355	
acc ttt atg tat gta ttt tct acg ttt gct aac ata ctg cgt aat aag	1203
Thr Phe Met Tyr Val Phe Ser Thr Phe Ala Asn Ile Leu Arg Asn Lys	
360 365 370	
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Glu Ser	
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<211> 64

<212> DNA

<213> Artificial Sequence

<220>

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 <223> a, t, c, g, other or unknown

<220>
 <221> modified_base
 <222> (38)
 <223> a, t, c, g, other or unknown

<220>
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 <222> (41)..(42)
 <223> a, t, c, g, other or unknown

<220>
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 <222> (44)..(45)
 <223> a, t, c, g, other or unknown

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 cgga 64

<210> 3
 <211> 71
 <212> DNA
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 <222> (19)..(20)
 <223> a, t, c, g, other or unknown

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 <222> (46)..(47)
 <223> a, t, c, g, other or unknown

<220>
 <221> modified_base
 <222> (52)..(53)
 <223> a, t, c, g, other or unknown

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 ttgacactct t 71

<210> 4
 <211> 74
 <212> DNA
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<220>

<223> Description of Artificial Sequence: Primer

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<222> (27)..(28)

<223> a, t, c, g, other or unknown

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<222> (33)..(34)

<223> a, t, c, g, other or unknown

<220>

<221> modified_base

<222> (42)..(43)

<223> a, t, c, g, other or unknown

<220>

<221> modified_base

<222> (54)..(55)

<223> a, t, c, g, other or unknown

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<210> 5

<211> 78

<212> DNA

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<223> Description of Artificial Sequence: Primer

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<223> a, t, c, g, other or unknown

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<222> (26)..(27)

<223> a, t, c, g, other or unknown

<220>

<221> modified_base

<222> (53)..(54)

<223> a, t, c, g, other or unknown

<220>

<221> modified_base

<222> (59)..(60)

<223> a, t, c, g, other or unknown

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gtatccgatg atgtagtt 78

<210> 6
 <211> 36
 <212> DNA
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<220>
 <223> Description of Artificial Sequence: Primer

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<210> 7
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 <212> DNA
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<220>
 <223> Description of Artificial Sequence: Primer

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<210> 8
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<220>
 <223> Description of Artificial Sequence: Synthetic
 oligodeoxynucleotide

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<210> 9
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<220>
 <223> Description of Artificial Sequence: Fragment of
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 <222> (22)..(84)

<220>
 <221> mat_peptide
 <222> (85)..(783)
 <223> fusion protein of bilin-binding protein, Strep-Tag II
 and albumin-binding domain

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<220>
<221> CDS
<222> (607)..(636)
<223> Strep-Tag II affinity tag
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<220>
<221> CDS
<222> (637)..(783)
<223> albumin binding domain from Protein G
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				Met	Lys	Lys	Thr	Ala	Ile	Ala	Ile	Ala	Val			
					-20					-15						
gca	ctg	gct	ggt	ttc	gct	acc	gta	gcg	cag	gcc	gac	gtg	tac	cac	gac	99
Ala	Leu	Ala	Gly	Phe	Ala	Thr	Val	Ala	Gln	Ala	Asp	Val	Tyr	His	Asp	
	-10					-5				-1	1				5	
ggt	gcc	tgt	ccc	gaa	gtc	aag	cca	gtc	gac	aac	ttc	gac	tgg	tcc	cag	147
Gly	Ala	Cys	Pro	Glu	Val	Lys	Pro	Val	Asp	Asn	Phe	Asp	Trp	Ser	Gln	
				10					15					20		
tac	cat	ggt	aaa	tgg	tgg	gaa	gtc	gcc	aaa	tac	ccc	aac	tca	gtt	gag	195
Tyr	His	Gly	Lys	Trp	Trp	Glu	Val	Ala	Lys	Tyr	Pro	Asn	Ser	Val	Glu	
			25					30					35			
aag	tac	gga	aag	tgc	gga	tgg	gct	gag	tac	act	cct	gaa	ggc	aag	agt	243
Lys	Tyr	Gly	Lys	Cys	Gly	Trp	Ala	Glu	Tyr	Thr	Pro	Glu	Gly	Lys	Ser	
		40					45					50				
gtc	aaa	gtt	tcg	aac	tac	cac	gta	atc	cac	ggc	aag	gaa	tac	ttt	att	291
Val	Lys	Val	Ser	Asn	Tyr	His	Val	Ile	His	Gly	Lys	Glu	Tyr	Phe	Ile	
	55					60					65					
gaa	gga	act	gcc	tac	cca	gtt	ggt	gac	tcc	aag	att	gga	aag	atc	tac	339
Glu	Gly	Thr	Ala	Tyr	Pro	Val	Gly	Asp	Ser	Lys	Ile	Gly	Lys	Ile	Tyr	
	70				75					80				85		
cac	agc	ctg	act	tac	gga	ggt	gtc	acc	aag	gag	aac	gta	ttc	aac	gta	387
His	Ser	Leu	Thr	Tyr	Gly	Gly	Val	Thr	Lys	Glu	Asn	Val	Phe	Asn	Val	
				90					95					100		
ctc	tcc	act	gac	aac	aag	aac	tac	atc	atc	gga	tac	tac	tgc	aaa	tac	435
Leu	Ser	Thr	Asp	Asn	Lys	Asn	Tyr	Ile	Ile	Gly	Tyr	Tyr	Cys	Lys	Tyr	
			105					110					115			
gac	gag	gac	aag	aag	gga	cac	caa	gac	ttc	gtc	tgg	gtg	ctc	tcc	aga	483
Asp	Glu	Asp	Lys	Lys	Gly	His	Gln	Asp	Phe	Val	Trp	Val	Leu	Ser	Arg	
		120					125					130				

agc atg gtc ctt act ggt gaa gcc aag acc gct gtc gag aac tac ctt 531
 Ser Met Val Leu Thr Gly Glu Ala Lys Thr Ala Val Glu Asn Tyr Leu
 135 140 145

atc ggc tcc cca gta gtc gac tcc cag aaa ctg gta tac agt gac ttc 579
 Ile Gly Ser Pro Val Val Asp Ser Gln Lys Leu Val Tyr Ser Asp Phe
 150 155 160 165

tct gaa gcc gcc tgc aag gtc aac aat agc aac tgg tct cac ccg cag 627
 Ser Glu Ala Ala Cys Lys Val Asn Asn Ser Asn Trp Ser His Pro Gln
 170 175 180

ttc gaa aaa cca gct agc ctg gct gaa gct aaa gtt ctg gct aac cgt 675
 Phe Glu Lys Pro Ala Ser Leu Ala Glu Ala Lys Val Leu Ala Asn Arg
 185 190 195

gaa ctg gac aaa tac ggt gtt tcc gac tac tac aaa aac ctc atc aac 723
 Glu Leu Asp Lys Tyr Gly Val Ser Asp Tyr Tyr Lys Asn Leu Ile Asn
 200 205 210

aac gct aaa acc gtt gaa ggt gtt aaa gct ctg atc gac gaa att ctc 771
 Asn Ala Lys Thr Val Glu Gly Val Lys Ala Leu Ile Asp Glu Ile Leu
 215 220 225

gca gca ctg ccg taataagctt 793
 Ala Ala Leu Pro
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<210> 10
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligodeoxynucleotide

<400> 10
 gacggtgcct gtcccga 17

<210> 11
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligodeoxynucleotide

<400> 11
 gactactggg gagccga 17

<210> 12
 <211> 522
 <212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: DigA nucleic acid sequence

<220>

<221> CDS

<222> (1)..(522)

<223> mutein DigA without fusion parts

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Asp Val Tyr His Asp Gly Ala Cys Pro Glu Val Lys Pro Val Asp Asn	
1 5 10 15	
ttc gac tgg tcc cag tac cat ggt aaa tgg tgg gaa gtc gcc aaa tac	96
Phe Asp Trp Ser Gln Tyr His Gly Lys Trp Trp Glu Val Ala Lys Tyr	
20 25 30	
ccc cat cac gag cgg aag tac gga aag tgc gga tgg gct gag tac act	144
Pro His His Glu Arg Lys Tyr Gly Lys Cys Gly Trp Ala Glu Tyr Thr	
35 40 45	
cct gaa ggc aag agt gtc aaa gtt tcg cgc tac tct gta atc cac ggc	192
Pro Glu Gly Lys Ser Val Lys Val Ser Arg Tyr Ser Val Ile His Gly	
50 55 60	
aag gaa tac ttt tcc gaa ggt acc gcc tac cca gtt ggt gac tcc aag	240
Lys Glu Tyr Phe Ser Glu Gly Thr Ala Tyr Pro Val Gly Asp Ser Lys	
65 70 75 80	
att gga aag atc tac cac agc tac act att gga ggt gtg acc cag gag	288
Ile Gly Lys Ile Tyr His Ser Tyr Thr Ile Gly Gly Val Thr Gln Glu	
85 90 95	
ggt gta ttc aac gta ctc tcc act gac aac aag aac tac atc atc gga	336
Gly Val Phe Asn Val Leu Ser Thr Asp Asn Lys Asn Tyr Ile Ile Gly	
100 105 110	
tac ttt tgc tcg tac gac gag gac aag aag gga cac atg gac ttg gtc	384
Tyr Phe Cys Ser Tyr Asp Glu Asp Lys Lys Gly His Met Asp Leu Val	
115 120 125	
tgg gtg ctc tcc aga agc atg gtc ctt act ggt gaa gcc aag acc gct	432
Trp Val Leu Ser Arg Ser Met Val Leu Thr Gly Glu Ala Lys Thr Ala	
130 135 140	
gtc gag aac tac ctt atc ggc tcc cca gta gtc gac tcc cag aaa ctg	480
Val Glu Asn Tyr Leu Ile Gly Ser Pro Val Val Asp Ser Gln Lys Leu	
145 150 155 160	
gta tac agt gac ttc tct gaa gcc gcc tgc aag gtc aac aat	522
Val Tyr Ser Asp Phe Ser Glu Ala Ala Cys Lys Val Asn Asn	
165 170	

<210> 13

<211> 76
 <212> DNA
 <213> Artificial Sequence

<220>
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 <223> a, t, c, g, t, other or unknown

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 <222> (53)..(54)
 <223> a, t, c, g, t, other or unknown

<220>
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 <222> (56)..(57)
 <223> a, t, c, g, t, other or unknown

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 gtacggaaag tgcgga 76

<210> 14
 <211> 1219
 <212> DNA
 <213> Artificial Sequence

<220>
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 pBBP24 nucleic acid sequence

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 <221> sig_peptide
 <222> (22)..(84)

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<223> fusion protein of bilin-binding protein, Strep-Tag II
and fragment of phage coat protein pIII, with
interrupted reading frame

<220>

<221> CDS

<222> (85..207, 214..606)

<223> mature bilin-binding protein with interrupted
reading frame

<220>

<221> CDS

<222> (607)..(636)

<223> Strep-Tag II affinity tag

<220>

<221> misc_feature

<222> (637)..(639)

<223> amber stop codon

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<221> CDS

<222> (640)..(1209)

<223> amino acids 217-406 of coat protein pIII

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gca ctg gct ggt ttc gct acc gta gcg cag gcc gac gtg tac cac gac	99
Ala Leu Ala Gly Phe Ala Thr Val Ala Gln Ala Asp Val Tyr His Asp	
-10 -5 -1 1 5	
ggt gcc tgt ccc gaa gtc aag cca gtc gac aac ttc gac tgg tcc cag	147
Gly Ala Cys Pro Glu Val Lys Pro Val Asn Phe Asp Trp Ser Gln	
10 15 20	
tac cat ggt aaa tgg tgg gaa gtc gcc aaa tac ccc aac tca gtt gag	195
Tyr His Gly Lys Trp Trp Glu Val Ala Lys Tyr Pro Asn Ser Val Glu	
25 30 35	
aag tac gga aat taatga tgg gct gag tac act cct gaa ggc aag agt	243
Lys Tyr Gly Asn Trp Ala Glu Tyr Thr Pro Glu Gly Lys Ser	
40 45 50	
gtc aaa gtt tcg aac tac cac gta atc cac ggc aag gaa tac ttt att	291
Val Lys Val Ser Asn Tyr His Val Ile His Gly Lys Glu Tyr Phe Ile	
55 60 65	
gaa gga act gcc tac cca gtt ggt gac tcc aag att gga aag atc tac	339
Glu Gly Thr Ala Tyr Pro Val Gly Asp Ser Lys Ile Gly Lys Ile Tyr	
70 75 80	
cac agc ctg act tac gga ggt gtc acc aag gag aac gta ttc aac gta	387
His Ser Leu Thr Tyr Gly Gly Val Thr Lys Glu Asn Val Phe Asn Val	
85 90 95	

ctc tcc act gac aac aag aac tac atc atc gga tac tac tgc aaa tac	435
Leu Ser Thr Asp Asn Lys Asn Tyr Ile Ile Gly Tyr Tyr Cys Lys Tyr	
100 105 110 115	
gac gag gac aag aag gga cac caa gac ttc gtc tgg gtg ctc tcc aga	483
Asp Glu Asp Lys Lys Gly His Gln Asp Phe Val Trp Val Leu Ser Arg	
120 125 130	
agc atg gtc ctt act ggt gaa gcc aag acc gct gtc gag aac tac ctt	531
Ser Met Val Leu Thr Gly Glu Ala Lys Thr Ala Val Glu Asn Tyr Leu	
135 140 145	
atc ggc tcc cca gta gtc gac tcc cag aaa ctg gta tac agt gac ttc	579
Ile Gly Ser Pro Val Val Asp Ser Gln Lys Leu Val Tyr Ser Asp Phe	
150 155 160	
tct gaa gcc gcc tgc aag gtc aac aat agc aac tgg tct cac ccg cag	627
Ser Glu Ala Ala Cys Lys Val Asn Asn Ser Asn Trp Ser His Pro Gln	
165 170 175	
ttc gaa aaa tag gct ggc ggc ggc tct ggt ggt ggt tct ggc ggc ggc	675
Phe Glu Lys Gln Ala Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly	
180 185 190 195	
tct gag ggt ggt ggc tct gag ggt ggc ggt tct gag ggt ggc ggc tct	723
Ser Glu Gly Gly Gly Ser Glu Gly Gly Ser Glu Gly Gly Gly Ser	
200 205 210	
gag gga ggc ggt tcc ggt ggt ggc tct ggt tcc ggt gat ttt gat tat	771
Glu Gly Gly Ser Gly Gly Gly Ser Gly Ser Gly Asp Phe Asp Tyr	
215 220 225	
gaa aag atg gca aac gct aat aag ggg gct atg acc gaa aat gcc gat	819
Glu Lys Met Ala Asn Ala Asn Lys Gly Ala Met Thr Glu Asn Ala Asp	
230 235 240	
gaa aac gcg cta cag tct gac gct aaa ggc aaa ctt gat tct gtc gct	867
Glu Asn Ala Leu Gln Ser Asp Ala Lys Gly Lys Leu Asp Ser Val Ala	
245 250 255	
act gat tac ggt gct gct atc gat ggt ttc att ggt gac gtt tcc ggc	915
Thr Asp Tyr Gly Ala Ala Ile Asp Gly Phe Ile Gly Asp Val Ser Gly	
260 265 270 275	
ctt gct aat ggt aat ggt gct act ggt gat ttt gct ggc tct aat tcc	963
Leu Ala Asn Gly Asn Gly Ala Thr Gly Asp Phe Ala Gly Ser Asn Ser	
280 285 290	
caa atg gct caa gtc ggt gac ggt gat aat tca cct tta atg aat aat	1011
Gln Met Ala Gln Val Gly Asp Gly Asp Asn Ser Pro Leu Met Asn Asn	
295 300 305	
ttc cgt caa tat tta cct tcc ctc cct caa tcg gtt gaa tgt cgc cct	1059
Phe Arg Gln Tyr Leu Pro Ser Leu Pro Gln Ser Val Glu Cys Arg Pro	
310 315 320	

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ttt gtc ttt ggc gct ggt aaa cca tat gaa ttt tct att gat tgt gac 1107
Phe Val Phe Gly Ala Gly Lys Pro Tyr Glu Phe Ser Ile Asp Cys Asp
325 330 335

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aaa ata aac tta ttc cgt ggt gtc ttt gcg ttt ctt tta tat gtt gcc 1155
Lys Ile Asn Leu Phe Arg Gly Val Phe Ala Phe Leu Leu Tyr Val Ala
340 345 350 355

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acc ttt atg tat gta ttt tct acg ttt gct aac ata ctg cgt aat aag 1203
Thr Phe Met Tyr Val Phe Ser Thr Phe Ala Asn Ile Leu Arg Asn Lys
360 365 370

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gag tct taataagctt 1219
Glu Ser

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<210> 15
<211> 522
<212> DNA
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence: Mutein DigA
nucleic acid sequence

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<220>
<221> CDS
<222> (1)..(522)
<223> mutein DigA16 without fusion parts

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Asp Val Tyr His Asp Gly Ala Cys Pro Glu Val Lys Pro Val Asp Asn
1 5 10 15

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ttc gac tgg tcc cag tac cat ggt aaa tgg tgg cag gtc gcc gcg tac 96
Phe Asp Trp Ser Gln Tyr His Gly Lys Trp Trp Gln Val Ala Ala Tyr
20 25 30

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ccc gat cat att acg aag tac gga aag tgc gga tgg gct gag tac act 144
Pro Asp His Ile Thr Lys Tyr Gly Lys Cys Gly Trp Ala Glu Tyr Thr
35 40 45

```

```

cct gaa ggc aag agt gtc aaa gtt tcg cgc tac tct gta atc cac ggc 192
Pro Glu Gly Lys Ser Val Lys Val Ser Arg Tyr Ser Val Ile His Gly
50 55 60

```

```

aag gaa tac ttt tcc gaa ggt acc gcc tac cca gtt ggt gac tcc aag 240
Lys Glu Tyr Phe Ser Glu Gly Thr Ala Tyr Pro Val Gly Asp Ser Lys
65 70 75 80

```

```

att gga aag atc tac cac agc tac act att gga ggt gtg acc cag gag 288
Ile Gly Lys Ile Tyr His Ser Tyr Thr Ile Gly Gly Val Thr Gln Glu
85 90 95

```

```

ggt gta ttc aac gta ctc tcc act gac aac aag aac tac atc atc gga 336
Gly Val Phe Asn Val Leu Ser Thr Asp Asn Lys Asn Tyr Ile Ile Gly
100 105 110

```

```

tac ttt tgc tcg tac gac gag gac aag aag gga cac atg gac ttg gtc 384
Tyr Phe Cys Ser Tyr Asp Glu Asp Lys Lys Gly His Met Asp Leu Val
      115                120                125

```

```

tgg gtg ctc tcc aga agc atg gtc ctt act ggt gaa gcc aag acc gct 432
Trp Val Leu Ser Arg Ser Met Val Leu Thr Gly Glu Ala Lys Thr Ala
      130                135                140

```

```

gtc gag aac tac ctt atc ggc tcc cca gta gtc gac tcc cag aaa ctg 480
Val Glu Asn Tyr Leu Ile Gly Ser Pro Val Val Asp Ser Gln Lys Leu
      145                150                155                160

```

```

gta tac agt gac ttc tct gaa gcc gcc tgc aag gtc aac aat 522
Val Tyr Ser Asp Phe Ser Glu Ala Ala Cys Lys Val Asn Asn
      165                170

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<210> 16

<211> 1380

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fragment of
pBBP21 nucleic acid sequence

<220>

<221> sig_peptide

<222> (22)..(84)

<220>

<221> mat_peptide

<222> (85)..(636)

<223> fusion protein of bilin-binding protein and Strep-Tag II

<220>

<221> sig_peptide

<222> (658)..(717)

<220>

<221> mat_peptide

<222> (718)..(1365)

<223> DsbC protein

<400> 16

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tctagataac gagggcaaaa a atg aaa aag aca gct atc gcg att gca gtg 51
                Met Lys Lys Thr Ala Ile Ala Ile Ala Val
                -20                -15

```

```

gca ctg gct ggt ttc gct acc gta gcg cag gcc gac gtg tac cac gac 99
Ala Leu Ala Gly Phe Ala Thr Val Ala Gln Ala Asp Val Tyr His Asp
      -10                -5                -1      1                5

```

```

ggt gcc tgt ccc gaa gtc aag cca gtc gac aac ttc gac tgg tcc cag 147
Gly Ala Cys Pro Glu Val Lys Pro Val Asp Asn Phe Asp Trp Ser Gln
      10                15                20

```

tac cat ggt aaa tgg tgg gaa gtc gcc aaa tac ccc aac tca gtt gag	195
Tyr His Gly Lys Trp Trp Glu Val Ala Lys Tyr Pro Asn Ser Val Glu	
25 30 35	
aag tac gga aag tgc gga tgg gct gag tac act cct gaa ggc aag agt	243
Lys Tyr Gly Lys Cys Gly Trp Ala Glu Tyr Thr Pro Glu Gly Lys Ser	
40 45 50	
gtc aaa gtt tcg aac tac cac gta atc cac ggc aag gaa tac ttt att	291
Val Lys Val Ser Asn Tyr His Val Ile His Gly Lys Glu Tyr Phe Ile	
55 60 65	
gaa gga act gcc tac cca gtt ggt gac tcc aag att gga aag atc tac	339
Glu Gly Thr Ala Tyr Pro Val Gly Asp Ser Lys Ile Gly Lys Ile Tyr	
70 75 80 85	
cac agc ctg act tac gga ggt gtc acc aag gag aac gta ttc aac gta	387
His Ser Leu Thr Tyr Gly Gly Val Thr Lys Glu Asn Val Phe Asn Val	
90 95 100	
ctc tcc act gac aac aag aac tac atc atc gga tac tac tgc aaa tac	435
Leu Ser Thr Asp Asn Lys Asn Tyr Ile Ile Gly Tyr Tyr Cys Lys Tyr	
105 110 115	
gac gag gac aag aag gga cac caa gac ttc gtc tgg gtg ctc tcc aga	483
Asp Glu Asp Lys Lys Gly His Gln Asp Phe Val Trp Val Leu Ser Arg	
120 125 130	
agc atg gtc ctt act ggt gaa gcc aag acc gct gtc gag aac tac ctt	531
Ser Met Val Leu Thr Gly Glu Ala Lys Thr Ala Val Glu Asn Tyr Leu	
135 140 145	
atc ggc tcc cca gta gtc gac tcc cag aaa ctg gta tac agt gac ttc	579
Ile Gly Ser Pro Val Val Asp Ser Gln Lys Leu Val Tyr Ser Asp Phe	
150 155 160 165	
tct gaa gcc gcc tgc aag gtc aac aat agc aac tgg tct cac ccg cag	627
Ser Glu Ala Ala Cys Lys Val Asn Asn Ser Asn Trp Ser His Pro Gln	
170 175 180	
ttc gaa aaa taataagctt cggaagatt t atg aag aaa ggt ttt atg ttg	678
Phe Glu Lys Met Lys Lys Gly Phe Met Leu	
-20 -15	
ttt act ttg tta gcg gcg ttt tca ggc ttt gct cag gct gat gac gcg	726
Phe Thr Leu Leu Ala Ala Phe Ser Gly Phe Ala Gln Ala Asp Asp Ala	
-10 -5 -1 1	
gca att caa caa acg tta gcc aaa atg ggc atc aaa agc agc gat att	774
Ala Ile Gln Gln Thr Leu Ala Lys Met Gly Ile Lys Ser Ser Asp Ile	
5 10 15	
cag ccc gcg cct gta gct ggc atg aag aca gtt ctg act aac agc ggc	822
Gln Pro Ala Pro Val Ala Gly Met Lys Thr Val Leu Thr Asn Ser Gly	
20 25 30 35	

gtg ttg tac atc acc gat gat ggt aaa cat atc att cag ggg cca atg	870
Val Leu Tyr Ile Thr Asp Asp Gly Lys His Ile Ile Gln Gly Pro Met	
40 45 50	
tat gac gtt agt ggc acg gct ccg gtc aat gtc acc aat aag atg ctg	918
Tyr Asp Val Ser Gly Thr Ala Pro Val Asn Val Thr Asn Lys Met Leu	
55 60 65	
tta aag cag ttg aat gcg ctt gaa aaa gag atg atc gtt tat aaa gcg	966
Leu Lys Gln Leu Asn Ala Leu Glu Lys Glu Met Ile Val Tyr Lys Ala	
70 75 80	
ccg cag gaa aaa cac gtc atc acc gtg ttt act gat att acc tgt ggt	1014
Pro Gln Glu Lys His Val Ile Thr Val Phe Thr Asp Ile Thr Cys Gly	
85 90 95	
tac tgc cac aaa ctg cat gag caa atg gca gac tac aac gcg ctg ggg	1062
Tyr Cys His Lys Leu His Glu Gln Met Ala Asp Tyr Asn Ala Leu Gly	
100 105 110 115	
atc acc gtg cgt tat ctt gct ttc ccg cgc cag ggg ctg gac agc gat	1110
Ile Thr Val Arg Tyr Leu Ala Phe Pro Arg Gln Gly Leu Asp Ser Asp	
120 125 130	
gca gag aaa gaa atg aaa gct atc tgg tgt gcg aaa gat aaa aac aaa	1158
Ala Glu Lys Glu Met Lys Ala Ile Trp Cys Ala Lys Asp Lys Asn Lys	
135 140 145	
gcg ttt gat gat gtg atg gca ggt aaa agc gtc gca cca gcc agt tgc	1206
Ala Phe Asp Asp Val Met Ala Gly Lys Ser Val Ala Pro Ala Ser Cys	
150 155 160	
gac gtg gat att gcc gac cat tac gca ctt ggc gtc cag ctt ggc gtt	1254
Asp Val Asp Ile Ala Asp His Tyr Ala Leu Gly Val Gln Leu Gly Val	
165 170 175	
agc ggt act ccg gca gtt gtg ctg agc aat ggc aca ctt gtt ccg ggt	1302
Ser Gly Thr Pro Ala Val Leu Ser Asn Gly Thr Leu Val Pro Gly	
180 185 190 195	
tac cag ccg ccg aaa gag atg aaa gaa ttc ctc gac gaa cac caa aaa	1350
Tyr Gln Pro Pro Lys Glu Met Lys Glu Phe Leu Asp Glu His Gln Lys	
200 205 210	
atg acc agc ggt aaa taattcgcgt agctt	1380
Met Thr Ser Gly Lys	
215	

<210> 17

<211> 2009

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fragment of
pBBP27 nucleic acid sequence

<220>
 <221> sig_peptide
 <222> (23)..(85)

<220>
 <221> mat_peptide
 <222> (86)..(1999)
 <223> fusion protein of alkaline phosphatase, linker peptide
 Pro-Pro-Ser-Ala, mutein DigA16 and Strep-Tag II

<220>
 <221> CDS
 <222> (86)..(1435)
 <223> mature part of alkaline phosphatase

<220>
 <221> CDS
 <222> (1436)..(1447)
 <223> linker peptide Pro-Pro-Ser-Ala

<220>
 <221> CDS
 <222> (1448)..(1969)
 <223> mutein DigA16

<220>
 <221> CDS
 <222> (1970)..(1999)
 <223> Strep-Tag II affinity tag

<400> 17

tctagaacat ggagaaaata aa gtg aaa caa agc act att gca ctg gca ctc	52
Val Lys Gln Ser Thr Ile Ala Leu Ala Leu	
-20 -15	
tta ccg tta ctg ttt acc cct gtg aca aaa gcc cgg aca cca gaa atg	100
Leu Pro Leu Leu Phe Thr Pro Val Thr Lys Ala Arg Thr Pro Glu Met	
-10 -5 -1 1 5	
cct gtt ctg gaa aac cgg gct gct cag ggc gat att act gca ccc ggc	148
Pro Val Leu Glu Asn Arg Ala Ala Gln Gly Asp Ile Thr Ala Pro Gly	
10 15 20	
ggg gct cgc cgt tta acg ggt gat cag act gcc gct ctg cgt gat tct	196
Gly Ala Arg Arg Leu Thr Gly Asp Gln Thr Ala Ala Leu Arg Asp Ser	
25 30 35	
ctt agc gat aaa cct gca aaa aat att att ttg ctg att ggc gat ggg	244
Leu Ser Asp Lys Pro Ala Lys Asn Ile Ile Leu Leu Ile Gly Asp Gly	
40 45 50	
atg ggg gac tcg gaa att act gcc gca cgt aat tat gcc gaa ggt gcg	292
Met Gly Asp Ser Glu Ile Thr Ala Ala Arg Asn Tyr Ala Glu Gly Ala	
55 60 65	
ggc ggc ttt ttt aaa ggt ata gat gcc tta ccg ctt acc ggg caa tac	340
Gly Gly Phe Phe Lys Gly Ile Asp Ala Leu Pro Leu Thr Gly Gln Tyr	
70 75 80 85	

act cac tat gcg ctg aat aaa aaa acc ggc aaa ccg gac tac gtc acc	388
Thr His Tyr Ala Leu Asn Lys Lys Thr Gly Lys Pro Asp Tyr Val Thr	
90 95 100	
gac tcg gct gca tca gca acc gcc tgg tca acc ggt gtc aaa acc tat	436
Asp Ser Ala Ala Ser Ala Thr Ala Trp Ser Thr Gly Val Lys Thr Tyr	
105 110 115	
aac ggc gcg ctg ggc gtc gat att cac gaa aaa gat cac cca acg att	484
Asn Gly Ala Leu Gly Val Asp Ile His Glu Lys Asp His Pro Thr Ile	
120 125 130	
ctg gaa atg gca aaa gcc gca ggt ctg gcg acc ggt aac gtt tct acc	532
Leu Glu Met Ala Lys Ala Ala Gly Leu Ala Thr Gly Asn Val Ser Thr	
135 140 145	
gca gag ttg cag gat gcc acg ccc gct gcg ctg gtg gca cat gtg acc	580
Ala Glu Leu Gln Asp Ala Thr Pro Ala Ala Leu Val Ala His Val Thr	
150 155 160 165	
tcg cgc aaa tgc tac ggt ccg agc gcg acc agt gaa aaa tgt ccg ggt	628
Ser Arg Lys Cys Tyr Gly Pro Ser Ala Thr Ser Glu Lys Cys Pro Gly	
170 175 180	
aac gct ctg gaa aaa ggc gga aaa gga tcg att acc gaa cag ctg ctt	676
Asn Ala Leu Glu Lys Gly Gly Lys Gly Ser Ile Thr Glu Gln Leu Leu	
185 190 195	
aac gct cgt gcc gac gtt acg ctt ggc ggc ggc gca aaa acc ttt gct	724
Asn Ala Arg Ala Asp Val Thr Leu Gly Gly Gly Ala Lys Thr Phe Ala	
200 205 210	
gaa acg gca acc gct ggt gaa tgg cag gga aaa acg ctg cgt gaa cag	772
Glu Thr Ala Thr Ala Gly Glu Trp Gln Gly Lys Thr Leu Arg Glu Gln	
215 220 225	
gca cag gcg cgt ggt tat cag ttg gtg agc gat gct gcc tca ctg aat	820
Ala Gln Ala Arg Gly Tyr Gln Leu Val Ser Asp Ala Ala Ser Leu Asn	
230 235 240 245	
tcg gtg acg gaa gcg aat cag caa aaa ccc ctg ctt ggc ctg ttt gct	868
Ser Val Thr Glu Ala Asn Gln Gln Lys Pro Leu Leu Gly Leu Phe Ala	
250 255 260	
gac ggc aat atg cca gtg cgc tgg cta gga ccg aaa gca acg tac cat	916
Asp Gly Asn Met Pro Val Arg Trp Leu Gly Pro Lys Ala Thr Tyr His	
265 270 275	
ggc aat atc gat aag ccc gca gtc acc tgt acg cca aat ccg caa cgt	964
Gly Asn Ile Asp Lys Pro Ala Val Thr Cys Thr Pro Asn Pro Gln Arg	
280 285 290	
aat gac agt gta cca acc ctg gcg cag atg acc gac aaa gcc att gaa	1012
Asn Asp Ser Val Pro Thr Leu Ala Gln Met Thr Asp Lys Ala Ile Glu	
295 300 305	

ttg ttg agt aaa aat gag aaa ggc ttt ttc ctg caa gtt gaa ggt gcg	1060
Leu Leu Ser Lys Asn Glu Lys Gly Phe Phe Leu Gln Val Glu Gly Ala	
310 315 320 325	
tca atc gat aaa cag gat cat gct gcg aat cct tgt ggg caa att ggc	1108
Ser Ile Asp Lys Gln Asp His Ala Ala Asn Pro Cys Gly Gln Ile Gly	
330 335 340	
gag acg gtc gat ctc gat gaa gcc gta caa cgg gcg ctg gaa ttc gct	1156
Glu Thr Val Asp Leu Asp Glu Ala Val Gln Arg Ala Leu Glu Phe Ala	
345 350 355	
aaa aag gag ggt aac acg ctg gtc ata gtc acc gct gat cac gcc cac	1204
Lys Lys Glu Gly Asn Thr Leu Val Ile Val Thr Ala Asp His Ala His	
360 365 370	
gcc agc cag att gtt gcg ccg gat acc aaa gct ccg ggc ctc acc cag	1252
Ala Ser Gln Ile Val Ala Pro Asp Thr Lys Ala Pro Gly Leu Thr Gln	
375 380 385	
gcg cta aat acc aaa gat ggc gca gtg atg gtg atg agt tac ggg aac	1300
Ala Leu Asn Thr Lys Asp Gly Ala Val Met Val Met Ser Tyr Gly Asn	
390 395 400 405	
tcc gaa gag gat tca caa gaa cat acc ggc agt cag ttg cgt att gcg	1348
Ser Glu Glu Asp Ser Gln Glu His Thr Gly Ser Gln Leu Arg Ile Ala	
410 415 420	
gcg tat ggc ccg cat gcc gcc aat gtt gtt gga ctg acc gac cag acc	1396
Ala Tyr Gly Pro His Ala Ala Asn Val Val Gly Leu Thr Asp Gln Thr	
425 430 435	
gat ctc ttc tac acc atg aaa gcc gct ctg ggg ctg aaa ccg cct agc	1444
Asp Leu Phe Tyr Thr Met Lys Ala Ala Leu Gly Leu Lys Pro Pro Ser	
440 445 450	
gct gac gtg tac cac gac ggt gcc tgt ccc gaa gtc aag cca gtc gac	1492
Ala Asp Val Tyr His Asp Gly Ala Cys Pro Glu Val Lys Pro Val Asp	
455 460 465	
aac ttc gac tgg tcc cag tac cat ggt aaa tgg tgg cag gtc gcc gcg	1540
Asn Phe Asp Trp Ser Gln Tyr His Gly Lys Trp Trp Gln Val Ala Ala	
470 475 480 485	
tac ccc gat cat att acg aag tac gga aag tgc gga tgg gct gag tac	1588
Tyr Pro Asp His Ile Thr Lys Tyr Gly Lys Cys Gly Trp Ala Glu Tyr	
490 495 500	
act cct gaa ggc aag agt gtc aaa gtt tgc cgc tac tct gta atc cac	1636
Thr Pro Glu Gly Lys Ser Val Lys Val Ser Arg Tyr Ser Val Ile His	
505 510 515	
ggc aag gaa tac ttt tcc gaa ggt acc gcc tac cca gtt ggt gac tcc	1684
Gly Lys Glu Tyr Phe Ser Glu Gly Thr Ala Tyr Pro Val Gly Asp Ser	
520 525 530	

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aag att gga aag atc tac cac agc tac act att gga ggt gtg acc cag 1732
Lys Ile Gly Lys Ile Tyr His Ser Tyr Thr Ile Gly Gly Val Thr Gln
535 540 545

gag ggt gta ttc aac gta ctc tcc act gac aac aag aac tac atc atc 1780
Glu Gly Val Phe Asn Val Leu Ser Thr Asp Asn Lys Asn Tyr Ile Ile
550 555 560 565

gga tac ttt tgc tcg tac gac gag gac aag aag gga cac atg gac ttg 1828
Gly Tyr Phe Cys Ser Tyr Asp Glu Asp Lys Lys Gly His Met Asp Leu
570 575 580

gtc tgg gtg ctc tcc aga agc atg gtc ctt act ggt gaa gcc aag acc 1876
Val Trp Val Leu Ser Arg Ser Met Val Leu Thr Gly Glu Ala Lys Thr
585 590 595

gct gtc gag aac tac ctt atc ggc tcc cca gta gtc gac tcc cag aaa 1924
Ala Val Glu Asn Tyr Leu Ile Gly Ser Pro Val Val Asp Ser Gln Lys
600 605 610

ctg gta tac agt gac ttc tct gaa gcc gcc tgc aag gtc aac aat agc 1972
Leu Val Tyr Ser Asp Phe Ser Glu Ala Ala Cys Lys Val Asn Asn Ser
615 620 625

aac tgg tct cac ccg cag ttc gaa aaa taataagctt 2009
Asn Trp Ser His Pro Gln Phe Glu Lys
630 635

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<210> 18

<211> 2005

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fragment of
pBBP29 nucleic acid sequence

<220>

<221> sig_peptide

<222> (22)..(84)

<220>

<221> mat_peptide

<222> (85)..(1998)

<223> fusion protein of mutein DigA16, Strep-Tag II, linker
peptide Gly(5) and alkaline phosphatase

<220>

<221> CDS

<222> (85)..(606)

<223> mutein DigA16

<220>

<221> CDS

<222> (607)..(636)

<223> Strep-Tag II affinity tag

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							Met	Lys	Lys	Thr	Ala	Ile	Ala	Ile	Ala	Val	
							-20								-15		
gca	ctg	gct	ggg	ttc	gct	acc	gta	gcg	cag	gcc	gac	gtg	tac	cac	gac	99	
Ala	Leu	Ala	Gly	Phe	Ala	Thr	Val	Ala	Gln	Ala	Asp	Val	Tyr	His	Asp		
			-10				-5				-1	1				5	
ggg	gcc	tgt	ccc	gaa	gtc	aag	cca	gtc	gac	aac	ttc	gac	tgg	tcc	cag	147	
Gly	Ala	Cys	Pro	Glu	Val	Lys	Pro	Val	Asp	Asn	Phe	Asp	Trp	Ser	Gln		
				10					15							20	
tac	cat	ggg	aaa	tgg	tgg	cag	gtc	gcc	gcg	tac	ccc	gat	cat	att	acg	195	
Tyr	His	Gly	Lys	Trp	Trp	Gln	Val	Ala	Ala	Tyr	Pro	Asp	His	Ile	Thr		
			25				30								35		
aag	tac	gga	aag	tgc	gga	tgg	gct	gag	tac	act	cct	gaa	ggc	aag	agt	243	
Lys	Tyr	Gly	Lys	Cys	Gly	Trp	Ala	Glu	Tyr	Thr	Pro	Glu	Gly	Lys	Ser		
			40				45								50		
gtc	aaa	gtt	tgc	cgc	tac	tct	gta	atc	cac	ggc	aag	gaa	tac	ttt	tcc	291	
Val	Lys	Val	Ser	Arg	Tyr	Ser	Val	Ile	His	Gly	Lys	Glu	Tyr	Phe	Ser		
			55				60								65		
gaa	ggg	acc	gcc	tac	cca	gtt	ggg	gac	tcc	aag	att	gga	aag	atc	tac	339	
Glu	Gly	Thr	Ala	Tyr	Pro	Val	Gly	Asp	Ser	Lys	Ile	Gly	Lys	Ile	Tyr		
		70				75				80						85	
cac	agc	tac	act	att	gga	ggg	gtg	acc	cag	gag	ggg	gta	ttc	aac	gta	387	
His	Ser	Tyr	Thr	Ile	Gly	Gly	Val	Thr	Gln	Glu	Gly	Val	Phe	Asn	Val		
			90				95								100		
ctc	tcc	act	gac	aac	aag	aac	tac	atc	atc	gga	tac	ttt	tgc	tgc	tac	435	
Leu	Ser	Thr	Asp	Asn	Lys	Asn	Tyr	Ile	Ile	Gly	Tyr	Phe	Cys	Ser	Tyr		
			105				110								115		
gac	gag	gac	aag	aag	gga	cac	atg	gac	ttg	gtc	tgg	gtg	ctc	tcc	aga	483	
Asp	Glu	Asp	Lys	Lys	Gly	His	Met	Asp	Leu	Val	Trp	Val	Leu	Ser	Arg		
			120				125								130		
agc	atg	gtc	ctt	act	ggg	gaa	gcc	aag	acc	gct	gtc	gag	aac	tac	ctt	531	
Ser	Met	Val	Leu	Thr	Gly	Glu	Ala	Lys	Thr	Ala	Val	Glu	Asn	Tyr	Leu		
		135				140								145			

atc ggc tcc cca gta gtc gac tcc cag aaa ctg gta tac agt gac ttc	579
Ile Gly Ser Pro Val Val Asp Ser Gln Lys Leu Val Tyr Ser Asp Phe	
150 155 160 165	
tct gaa gcc gcc tgc aag gtc aac aat agc aac tgg tct cac ccg cag	627
Ser Glu Ala Ala Cys Lys Val Asn Asn Ser Asn Trp Ser His Pro Gln	
170 175 180	
ttc gaa aaa ggt ggc ggc ggt ggt aca cca gaa atg cct gtt ctg gaa	675
Phe Glu Lys Gly Gly Gly Gly Gly Thr Pro Glu Met Pro Val Leu Glu	
185 190 195	
aac cgg gct gct cag ggc gat att act gca ccc ggc ggt gct cgc cgt	723
Asn Arg Ala Ala Gln Gly Asp Ile Thr Ala Pro Gly Gly Ala Arg Arg	
200 205 210	
tta acg ggt gat cag act gcc gct ctg cgt gat tct ctt agc gat aaa	771
Leu Thr Gly Asp Gln Thr Ala Ala Leu Arg Asp Ser Leu Ser Asp Lys	
215 220 225	
cct gca aaa aat att att ttg ctg att ggc gat ggg atg ggg gac tcg	819
Pro Ala Lys Asn Ile Ile Leu Leu Ile Gly Asp Gly Met Gly Asp Ser	
230 235 240 245	
gaa att act gcc gca cgt aat tat gcc gaa ggt gcg ggc ggc ttt ttt	867
Glu Ile Thr Ala Ala Arg Asn Tyr Ala Glu Gly Ala Gly Gly Phe Phe	
250 255 260	
aaa ggt ata gat gcc tta ccg ctt acc ggg caa tac act cac tat gcg	915
Lys Gly Ile Asp Ala Leu Pro Leu Thr Gly Gln Tyr Thr His Tyr Ala	
265 270 275	
ctg aat aaa aaa acc ggc aaa ccg gac tac gtc acc gac tcg gct gca	963
Leu Asn Lys Lys Thr Gly Lys Pro Asp Tyr Val Thr Asp Ser Ala Ala	
280 285 290	
tca gca acc gcc tgg tca acc ggt gtc aaa acc tat aac ggc gcg ctg	1011
Ser Ala Thr Ala Trp Ser Thr Gly Val Lys Thr Tyr Asn Gly Ala Leu	
295 300 305	
ggc gtc gat att cac gaa aaa gat cac cca acg att ctg gaa atg gca	1059
Gly Val Asp Ile His Glu Lys Asp His Pro Thr Ile Leu Glu Met Ala	
310 315 320 325	
aaa gcc gca ggt ctg gcg acc ggt aac gtt tct acc gca gag ttg cag	1107
Lys Ala Ala Gly Leu Ala Thr Gly Asn Val Ser Thr Ala Glu Leu Gln	
330 335 340	
gat gcc acg ccc gct gcg ctg gtg gca cat gtg acc tcg cgc aaa tgc	1155
Asp Ala Thr Pro Ala Ala Leu Val Ala His Val Thr Ser Arg Lys Cys	
345 350 355	
tac ggt ccg agc gcg acc agt gaa aaa tgt ccg ggt aac gct ctg gaa	1203
Tyr Gly Pro Ser Ala Thr Ser Glu Lys Cys Pro Gly Asn Ala Leu Glu	
360 365 370	

aaa ggc gga aaa gga tcg att acc gaa cag ctg ctt aac gct cgt gcc	1251
Lys Gly Gly Lys Gly Ser Ile Thr Glu Gln Leu Leu Asn Ala Arg Ala	
375 380 385	
gac gtt acg ctt ggc ggc ggc gca aaa acc ttt gct gaa acg gca acc	1299
Asp Val Thr Leu Gly Gly Gly Ala Lys Thr Phe Ala Glu Thr Ala Thr	
390 395 400 405	
gct ggt gaa tgg cag gga aaa acg ctg cgt gaa cag gca cag gcg cgt	1347
Ala Gly Glu Trp Gln Gly Lys Thr Leu Arg Glu Gln Ala Gln Ala Arg	
410 415 420	
ggc tat cag ttg gtg agc gat gct gcc tca ctg aat tcg gtg acg gaa	1395
Gly Tyr Gln Leu Val Ser Asp Ala Ala Ser Leu Asn Ser Val Thr Glu	
425 430 435	
gcg aat cag caa aaa ccc ctg ctt ggc ctg ttt gct gac ggc aat atg	1443
Ala Asn Gln Gln Lys Pro Leu Leu Gly Leu Phe Ala Asp Gly Asn Met	
440 445 450	
cca gtg cgc tgg cta gga ccg aaa gca acg tac cat ggc aat atc gat	1491
Pro Val Arg Trp Leu Gly Pro Lys Ala Thr Tyr His Gly Asn Ile Asp	
455 460 465	
aag ccc gca gtc acc tgt acg cca aat ccg caa cgt aat gac agt gta	1539
Lys Pro Ala Val Thr Cys Thr Pro Asn Pro Gln Arg Asn Asp Ser Val	
470 475 480 485	
cca acc ctg gcg cag atg acc gac aaa gcc att gaa ttg ttg agt aaa	1587
Pro Thr Leu Ala Gln Met Thr Asp Lys Ala Ile Glu Leu Leu Ser Lys	
490 495 500	
aat gag aaa ggc ttt ttc ctg caa gtt gaa ggt gcg tca atc gat aaa	1635
Asn Glu Lys Gly Phe Phe Leu Gln Val Glu Gly Ala Ser Ile Asp Lys	
505 510 515	
cag gat cat gct gcg aat cct tgt ggg caa att ggc gag acg gtc gat	1683
Gln Asp His Ala Ala Asn Pro Cys Gly Gln Ile Gly Glu Thr Val Asp	
520 525 530	
ctc gat gaa gcc gta caa cgg gcg ctg gaa ttc gct aaa aag gag ggt	1731
Leu Asp Glu Ala Val Gln Arg Ala Leu Glu Phe Ala Lys Lys Glu Gly	
535 540 545	
aac acg ctg gtc ata gtc acc gct gat cac gcc cac gcc agc cag att	1779
Asn Thr Leu Val Ile Val Thr Ala Asp His Ala His Ala Ser Gln Ile	
550 555 560 565	
gtt gcg ccg gat acc aaa gct ccg ggc ctc acc cag gcg cta aat acc	1827
Val Ala Pro Asp Thr Lys Ala Pro Gly Leu Thr Gln Ala Leu Asn Thr	
570 575 580	
aaa gat ggc gca gtg atg gtg atg agt tac ggg aac tcc gaa gag gat	1875
Lys Asp Gly Ala Val Met Val Met Ser Tyr Gly Asn Ser Glu Glu Asp	
585 590 595	

tca caa gaa cat acc ggc agt cag ttg cgt att gcg gcg tat ggc ccg 1923
Ser Gln Glu His Thr Gly Ser Gln Leu Arg Ile Ala Ala Tyr Gly Pro
600 605 610

cat gcc gcc aat gtt gtt gga ctg acc gac cag acc gat ctc ttc tac 1971
His Ala Ala Asn Val Val Gly Leu Thr Asp Gln Thr Asp Leu Phe Tyr
615 620 625

acc atg aaa gcc gct ctg ggg ctg aaa taagctt 2005
Thr Met Lys Ala Ala Leu Gly Leu Lys
630 635

<210> 19

<211> 396

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: pBBP20
amino acid sequence

<400> 19

Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala
-20 -15 -10

Thr Val Ala Gln Ala Asp Val Tyr His Asp Gly Ala Cys Pro Glu Val
-5 -1 1 5 10

Lys Pro Val Asp Asn Phe Asp Trp Ser Gln Tyr His Gly Lys Trp Trp
15 20 25

Glu Val Ala Lys Tyr Pro Asn Ser Val Glu Lys Tyr Gly Lys Cys Gly
30 35 40

Trp Ala Glu Tyr Thr Pro Glu Gly Lys Ser Val Lys Val Ser Asn Tyr
45 50 55

His Val Ile His Gly Lys Glu Tyr Phe Ile Glu Gly Thr Ala Tyr Pro
60 65 70 75

Val Gly Asp Ser Lys Ile Gly Lys Ile Tyr His Ser Leu Thr Tyr Gly
80 85 90

Gly Val Thr Lys Glu Asn Val Phe Asn Val Leu Ser Thr Asp Asn Lys
95 100 105

Asn Tyr Ile Ile Gly Tyr Tyr Cys Lys Tyr Asp Glu Asp Lys Lys Gly
110 115 120

His Gln Asp Phe Val Trp Val Leu Ser Arg Ser Met Val Leu Thr Gly
125 130 135

Glu Ala Lys Thr Ala Val Glu Asn Tyr Leu Ile Gly Ser Pro Val Val
140 145 150 155

Asp Ser Gln Lys Leu Val Tyr Ser Asp Phe Ser Glu Ala Ala Cys Lys
160 165 170

Val Asn Asn Ser Asn Trp Ser His Pro Gln Phe Glu Lys Lys Ala Gly
 175 180 185
 Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu Gly Gly Gly Ser
 190 195 200
 Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Gly
 205 210 215
 Gly Gly Ser Gly Ser Gly Asp Phe Asp Tyr Glu Lys Met Ala Asn Ala
 220 225 230 235
 Asn Lys Gly Ala Met Thr Glu Asn Ala Asp Glu Asn Ala Leu Gln Ser
 240 245 250
 Asp Ala Lys Gly Lys Leu Asp Ser Val Ala Thr Asp Tyr Gly Ala Ala
 255 260 265
 Ile Asp Gly Phe Ile Gly Asp Val Ser Gly Leu Ala Asn Gly Asn Gly
 270 275 280
 Ala Thr Gly Asp Phe Ala Gly Ser Asn Ser Gln Met Ala Gln Val Gly
 285 290 295
 Asp Gly Asp Asn Ser Pro Leu Met Asn Asn Phe Arg Gln Tyr Leu Pro
 300 305 310 315
 Ser Leu Pro Gln Ser Val Glu Cys Arg Pro Phe Val Phe Gly Ala Gly
 320 325 330
 Lys Pro Tyr Glu Phe Ser Ile Asp Cys Asp Lys Ile Asn Leu Phe Arg
 335 340 345
 Gly Val Phe Ala Phe Leu Leu Tyr Val Ala Thr Phe Met Tyr Val Phe
 350 355 360
 Ser Thr Phe Ala Asn Ile Leu Arg Asn Lys Glu Ser
 365 370 375

<210> 20

<211> 254

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fragment of
pBBP22 amino acid sequence

<400> 20

Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala
 -20 -15 -10

Thr Val Ala Gln Ala Asp Val Tyr His Asp Gly Ala Cys Pro Glu Val
 -5 -1 1 5 10

Lys Pro Val Asp Asn Phe Asp Trp Ser Gln Tyr His Gly Lys Trp Trp
 15 20 25
 Glu Val Ala Lys Tyr Pro Asn Ser Val Glu Lys Tyr Gly Lys Cys Gly
 30 35 40
 Trp Ala Glu Tyr Thr Pro Glu Gly Lys Ser Val Lys Val Ser Asn Tyr
 45 50 55
 His Val Ile His Gly Lys Glu Tyr Phe Ile Glu Gly Thr Ala Tyr Pro
 60 65 70 75
 Val Gly Asp Ser Lys Ile Gly Lys Ile Tyr His Ser Leu Thr Tyr Gly
 80 85 90
 Gly Val Thr Lys Glu Asn Val Phe Asn Val Leu Ser Thr Asp Asn Lys
 95 100 105
 Asn Tyr Ile Ile Gly Tyr Tyr Cys Lys Tyr Asp Glu Asp Lys Lys Gly
 110 115 120
 His Gln Asp Phe Val Trp Val Leu Ser Arg Ser Met Val Leu Thr Gly
 125 130 135
 Glu Ala Lys Thr Ala Val Glu Asn Tyr Leu Ile Gly Ser Pro Val Val
 140 145 150 155
 Asp Ser Gln Lys Leu Val Tyr Ser Asp Phe Ser Glu Ala Ala Cys Lys
 160 165 170
 Val Asn Asn Ser Asn Trp Ser His Pro Gln Phe Glu Lys Pro Ala Ser
 175 180 185
 Leu Ala Glu Ala Lys Val Leu Ala Asn Arg Glu Leu Asp Lys Tyr Gly
 190 195 200
 Val Ser Asp Tyr Tyr Lys Asn Leu Ile Asn Asn Ala Lys Thr Val Glu
 205 210 215
 Gly Val Lys Ala Leu Ile Asp Glu Ile Leu Ala Ala Leu Pro
 220 225 230

<210> 21

<211> 174

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: DigA amino acid sequence

<400> 21

Asp Val Tyr His Asp Gly Ala Cys Pro Glu Val Lys Pro Val Asp Asn
 1 5 10 15
 Phe Asp Trp Ser Gln Tyr His Gly Lys Trp Trp Glu Val Ala Lys Tyr
 20 25 30

```

Pro His His Glu Arg Lys Tyr Gly Lys Cys Gly Trp Ala Glu Tyr Thr
      35              40              45

Pro Glu Gly Lys Ser Val Lys Val Ser Arg Tyr Ser Val Ile His Gly
      50              55              60

Lys Glu Tyr Phe Ser Glu Gly Thr Ala Tyr Pro Val Gly Asp Ser Lys
      65              70              75              80

Ile Gly Lys Ile Tyr His Ser Tyr Thr Ile Gly Gly Val Thr Gln Glu
      85              90              95

Gly Val Phe Asn Val Leu Ser Thr Asp Asn Lys Asn Tyr Ile Ile Gly
      100             105             110

Tyr Phe Cys Ser Tyr Asp Glu Asp Lys Lys Gly His Met Asp Leu Val
      115             120             125

Trp Val Leu Ser Arg Ser Met Val Leu Thr Gly Glu Ala Lys Thr Ala
      130             135             140

Val Glu Asn Tyr Leu Ile Gly Ser Pro Val Val Asp Ser Gln Lys Leu
      145             150             155             160

Val Tyr Ser Asp Phe Ser Glu Ala Ala Cys Lys Val Asn Asn
      165             170

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<210> 22

<211> 394

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fragment of
pBBP24 amino acid sequence

<400> 22

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Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala
      -20              -15              -10

```

```

Thr Val Ala Gln Ala Asp Val Tyr His Asp Gly Ala Cys Pro Glu Val
      -5              -1      1              5              10

```

```

Lys Pro Val Asp Asn Phe Asp Trp Ser Gln Tyr His Gly Lys Trp Trp
      15              20              25

```

```

Glu Val Ala Lys Tyr Pro Asn Ser Val Glu Lys Tyr Gly Asn Trp Ala
      30              35              40

```

```

Glu Tyr Thr Pro Glu Gly Lys Ser Val Lys Val Ser Asn Tyr His Val
      45              50              55

```

```

Ile His Gly Lys Glu Tyr Phe Ile Glu Gly Thr Ala Tyr Pro Val Gly
      60              65              70              75

```

Asp Ser Lys Ile Gly Lys Ile Tyr His Ser Leu Thr Tyr Gly Gly Val
 80 85 90
 Thr Lys Glu Asn Val Phe Asn Val Leu Ser Thr Asp Asn Lys Asn Tyr
 95 100 105
 Ile Ile Gly Tyr Tyr Cys Lys Tyr Asp Glu Asp Lys Lys Gly His Gln
 110 115 120
 Asp Phe Val Trp Val Leu Ser Arg Ser Met Val Leu Thr Gly Glu Ala
 125 130 135
 Lys Thr Ala Val Glu Asn Tyr Leu Ile Gly Ser Pro Val Val Asp Ser
 140 145 150 155
 Gln Lys Leu Val Tyr Ser Asp Phe Ser Glu Ala Ala Cys Lys Val Asn
 160 165 170
 Asn Ser Asn Trp Ser His Pro Gln Phe Glu Lys Lys Ala Gly Gly Gly
 175 180 185
 Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly
 190 195 200
 Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Gly Gly Gly
 205 210 215
 Ser Gly Ser Gly Asp Phe Asp Tyr Glu Lys Met Ala Asn Ala Asn Lys
 220 225 230 235
 Gly Ala Met Thr Glu Asn Ala Asp Glu Asn Ala Leu Gln Ser Asp Ala
 240 245 250
 Lys Gly Lys Leu Asp Ser Val Ala Thr Asp Tyr Gly Ala Ala Ile Asp
 255 260 265
 Gly Phe Ile Gly Asp Val Ser Gly Leu Ala Asn Gly Asn Gly Ala Thr
 270 275 280
 Gly Asp Phe Ala Gly Ser Asn Ser Gln Met Ala Gln Val Gly Asp Gly
 285 290 295
 Asp Asn Ser Pro Leu Met Asn Asn Phe Arg Gln Tyr Leu Pro Ser Leu
 300 305 310 315
 Pro Gln Ser Val Glu Cys Arg Pro Phe Val Phe Gly Ala Gly Lys Pro
 320 325 330
 Tyr Glu Phe Ser Ile Asp Cys Asp Lys Ile Asn Leu Phe Arg Gly Val
 335 340 345
 Phe Ala Phe Leu Leu Tyr Val Ala Thr Phe Met Tyr Val Phe Ser Thr
 350 355 360
 Phe Ala Asn Ile Leu Arg Asn Lys Glu Ser
 365 370

<210> 23
 <211> 174
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Mutein DigA16
 amino acid sequence

<400> 23
 Asp Val Tyr His Asp Gly Ala Cys Pro Glu Val Lys Pro Val Asp Asn
 1 5 10 15
 Phe Asp Trp Ser Gln Tyr His Gly Lys Trp Trp Gln Val Ala Ala Tyr
 20 25 30
 Pro Asp His Ile Thr Lys Tyr Gly Lys Cys Gly Trp Ala Glu Tyr Thr
 35 40 45
 Pro Glu Gly Lys Ser Val Lys Val Ser Arg Tyr Ser Val Ile His Gly
 50 55 60
 Lys Glu Tyr Phe Ser Glu Gly Thr Ala Tyr Pro Val Gly Asp Ser Lys
 65 70 75 80
 Ile Gly Lys Ile Tyr His Ser Tyr Thr Ile Gly Gly Val Thr Gln Glu
 85 90 95
 Gly Val Phe Asn Val Leu Ser Thr Asp Asn Lys Asn Tyr Ile Ile Gly
 100 105 110
 Tyr Phe Cys Ser Tyr Asp Glu Asp Lys Lys Gly His Met Asp Leu Val
 115 120 125
 Trp Val Leu Ser Arg Ser Met Val Leu Thr Gly Glu Ala Lys Thr Ala
 130 135 140
 Val Glu Asn Tyr Leu Ile Gly Ser Pro Val Val Asp Ser Gln Lys Leu
 145 150 155 160
 Val Tyr Ser Asp Phe Ser Glu Ala Ala Cys Lys Val Asn Asn
 165 170

<210> 24
 <211> 205
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Fragment of
 pBBP21 amino acid sequence

<400> 24
 Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala
 -20 -15 -10

```

Thr Val Ala Gln Ala Asp Val Tyr His Asp Gly Ala Cys Pro Glu Val
-5          -1  1          5          10

Lys Pro Val Asp Asn Phe Asp Trp Ser Gln Tyr His Gly Lys Trp Trp
          15          20          25

Glu Val Ala Lys Tyr Pro Asn Ser Val Glu Lys Tyr Gly Lys Cys Gly
          30          35          40

Trp Ala Glu Tyr Thr Pro Glu Gly Lys Ser Val Lys Val Ser Asn Tyr
          45          50          55

His Val Ile His Gly Lys Glu Tyr Phe Ile Glu Gly Thr Ala Tyr Pro
          60          65          70          75

Val Gly Asp Ser Lys Ile Gly Lys Ile Tyr His Ser Leu Thr Tyr Gly
          80          85          90

Gly Val Thr Lys Glu Asn Val Phe Asn Val Leu Ser Thr Asp Asn Lys
          95          100          105

Asn Tyr Ile Ile Gly Tyr Tyr Cys Lys Tyr Asp Glu Asp Lys Lys Gly
          110          115          120

His Gln Asp Phe Val Trp Val Leu Ser Arg Ser Met Val Leu Thr Gly
          125          130          135

Glu Ala Lys Thr Ala Val Glu Asn Tyr Leu Ile Gly Ser Pro Val Val
          140          145          150          155

Asp Ser Gln Lys Leu Val Tyr Ser Asp Phe Ser Glu Ala Ala Cys Lys
          160          165          170

Val Asn Asn Ser Asn Trp Ser His Pro Gln Phe Glu Lys
          175          180

```

<210> 25

<211> 236

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fragment of
pBBP21 amino acid sequence

<400> 25

```

Met Lys Lys Gly Phe Met Leu Phe Thr Leu Leu Ala Ala Phe Ser Gly
-20          -15          -10          -5

Phe Ala Gln Ala Asp Asp Ala Ala Ile Gln Gln Thr Leu Ala Lys Met
          -1  1          5          10

Gly Ile Lys Ser Ser Asp Ile Gln Pro Ala Pro Val Ala Gly Met Lys
          15          20          25

Thr Val Leu Thr Asn Ser Gly Val Leu Tyr Ile Thr Asp Asp Gly Lys
          30          35          40

```

His Ile Ile Gln Gly Pro Met Tyr Asp Val Ser Gly Thr Ala Pro Val
 45 50 55 60
 Asn Val Thr Asn Lys Met Leu Leu Lys Gln Leu Asn Ala Leu Glu Lys
 65 70 75
 Glu Met Ile Val Tyr Lys Ala Pro Gln Glu Lys His Val Ile Thr Val
 80 85 90
 Phe Thr Asp Ile Thr Cys Gly Tyr Cys His Lys Leu His Glu Gln Met
 95 100 105
 Ala Asp Tyr Asn Ala Leu Gly Ile Thr Val Arg Tyr Leu Ala Phe Pro
 110 115 120
 Arg Gln Gly Leu Asp Ser Asp Ala Glu Lys Glu Met Lys Ala Ile Trp
 125 130 135 140
 Cys Ala Lys Asp Lys Asn Lys Ala Phe Asp Asp Val Met Ala Gly Lys
 145 150 155
 Ser Val Ala Pro Ala Ser Cys Asp Val Asp Ile Ala Asp His Tyr Ala
 160 165 170
 Leu Gly Val Gln Leu Gly Val Ser Gly Thr Pro Ala Val Val Leu Ser
 175 180 185
 Asn Gly Thr Leu Val Pro Gly Tyr Gln Pro Pro Lys Glu Met Lys Glu
 190 195 200
 Phe Leu Asp Glu His Gln Lys Met Thr Ser Gly Lys
 205 210 215

<210> 26

<211> 659

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fragment of
pBBP27 amino acid sequence

<400> 26

Val Lys Gln Ser Thr Ile Ala Leu Ala Leu Leu Pro Leu Leu Phe Thr
 -20 -15 -10
 Pro Val Thr Lys Ala Arg Thr Pro Glu Met Pro Val Leu Glu Asn Arg
 -5 -1 1 5 10
 Ala Ala Gln Gly Asp Ile Thr Ala Pro Gly Gly Ala Arg Arg Leu Thr
 15 20 25
 Gly Asp Gln Thr Ala Ala Leu Arg Asp Ser Leu Ser Asp Lys Pro Ala
 30 35 40

Lys Asn Ile Ile Leu Leu Ile Gly Asp Gly Met Gly Asp Ser Glu Ile
 45 50 55
 Thr Ala Ala Arg Asn Tyr Ala Glu Gly Ala Gly Gly Phe Phe Lys Gly
 60 65 70 75
 Ile Asp Ala Leu Pro Leu Thr Gly Gln Tyr Thr His Tyr Ala Leu Asn
 80 85 90
 Lys Lys Thr Gly Lys Pro Asp Tyr Val Thr Asp Ser Ala Ala Ser Ala
 95 100 105
 Thr Ala Trp Ser Thr Gly Val Lys Thr Tyr Asn Gly Ala Leu Gly Val
 110 115 120
 Asp Ile His Glu Lys Asp His Pro Thr Ile Leu Glu Met Ala Lys Ala
 125 130 135
 Ala Gly Leu Ala Thr Gly Asn Val Ser Thr Ala Glu Leu Gln Asp Ala
 140 145 150 155
 Thr Pro Ala Ala Leu Val Ala His Val Thr Ser Arg Lys Cys Tyr Gly
 160 165 170
 Pro Ser Ala Thr Ser Glu Lys Cys Pro Gly Asn Ala Leu Glu Lys Gly
 175 180 185
 Gly Lys Gly Ser Ile Thr Glu Gln Leu Leu Asn Ala Arg Ala Asp Val
 190 195 200
 Thr Leu Gly Gly Gly Ala Lys Thr Phe Ala Glu Thr Ala Thr Ala Gly
 205 210 215
 Glu Trp Gln Gly Lys Thr Leu Arg Glu Gln Ala Gln Ala Arg Gly Tyr
 220 225 230 235
 Gln Leu Val Ser Asp Ala Ala Ser Leu Asn Ser Val Thr Glu Ala Asn
 240 245 250
 Gln Gln Lys Pro Leu Leu Gly Leu Phe Ala Asp Gly Asn Met Pro Val
 255 260 265
 Arg Trp Leu Gly Pro Lys Ala Thr Tyr His Gly Asn Ile Asp Lys Pro
 270 275 280
 Ala Val Thr Cys Thr Pro Asn Pro Gln Arg Asn Asp Ser Val Pro Thr
 285 290 295
 Leu Ala Gln Met Thr Asp Lys Ala Ile Glu Leu Leu Ser Lys Asn Glu
 300 305 310 315
 Lys Gly Phe Phe Leu Gln Val Glu Gly Ala Ser Ile Asp Lys Gln Asp
 320 325 330
 His Ala Ala Asn Pro Cys Gly Gln Ile Gly Glu Thr Val Asp Leu Asp
 335 340 345

Glu Ala Val Gln Arg Ala Leu Glu Phe Ala Lys Lys Glu Gly Asn Thr
 350 355 360
 Leu Val Ile Val Thr Ala Asp His Ala His Ala Ser Gln Ile Val Ala
 365 370 375
 Pro Asp Thr Lys Ala Pro Gly Leu Thr Gln Ala Leu Asn Thr Lys Asp
 380 385 390 395
 Gly Ala Val Met Val Met Ser Tyr Gly Asn Ser Glu Glu Asp Ser Gln
 400 405 410
 Glu His Thr Gly Ser Gln Leu Arg Ile Ala Ala Tyr Gly Pro His Ala
 415 420 425
 Ala Asn Val Val Gly Leu Thr Asp Gln Thr Asp Leu Phe Tyr Thr Met
 430 435 440
 Lys Ala Ala Leu Gly Leu Lys Pro Pro Ser Ala Asp Val Tyr His Asp
 445 450 455
 Gly Ala Cys Pro Glu Val Lys Pro Val Asp Asn Phe Asp Trp Ser Gln
 460 465 470 475
 Tyr His Gly Lys Trp Trp Gln Val Ala Ala Tyr Pro Asp His Ile Thr
 480 485 490
 Lys Tyr Gly Lys Cys Gly Trp Ala Glu Tyr Thr Pro Glu Gly Lys Ser
 495 500 505
 Val Lys Val Ser Arg Tyr Ser Val Ile His Gly Lys Glu Tyr Phe Ser
 510 515 520
 Glu Gly Thr Ala Tyr Pro Val Gly Asp Ser Lys Ile Gly Lys Ile Tyr
 525 530 535
 His Ser Tyr Thr Ile Gly Gly Val Thr Gln Glu Gly Val Phe Asn Val
 540 545 550 555
 Leu Ser Thr Asp Asn Lys Asn Tyr Ile Ile Gly Tyr Phe Cys Ser Tyr
 560 565 570
 Asp Glu Asp Lys Lys Gly His Met Asp Leu Val Trp Val Leu Ser Arg
 575 580 585
 Ser Met Val Leu Thr Gly Glu Ala Lys Thr Ala Val Glu Asn Tyr Leu
 590 595 600
 Ile Gly Ser Pro Val Val Asp Ser Gln Lys Leu Val Tyr Ser Asp Phe
 605 610 615
 Ser Glu Ala Ala Cys Lys Val Asn Asn Ser Asn Trp Ser His Pro Gln
 620 625 630 635
 Phe Glu Lys

<211> 659

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fragment of
pBBP29 amino acid sequence

<400> 27

```

Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala
  -20                -15                -10

Thr Val Ala Gln Ala Asp Val Tyr His Asp Gly Ala Cys Pro Glu Val
  -5                -1   1                5                10

Lys Pro Val Asp Asn Phe Asp Trp Ser Gln Tyr His Gly Lys Trp Trp
          15                20                25

Gln Val Ala Ala Tyr Pro Asp His Ile Thr Lys Tyr Gly Lys Cys Gly
          30                35                40

Trp Ala Glu Tyr Thr Pro Glu Gly Lys Ser Val Lys Val Ser Arg Tyr
          45                50                55

Ser Val Ile His Gly Lys Glu Tyr Phe Ser Glu Gly Thr Ala Tyr Pro
          60                65                70                75

Val Gly Asp Ser Lys Ile Gly Lys Ile Tyr His Ser Tyr Thr Ile Gly
          80                85                90

Gly Val Thr Gln Glu Gly Val Phe Asn Val Leu Ser Thr Asp Asn Lys
          95                100               105

Asn Tyr Ile Ile Gly Tyr Phe Cys Ser Tyr Asp Glu Asp Lys Lys Gly
          110               115               120

His Met Asp Leu Val Trp Val Leu Ser Arg Ser Met Val Leu Thr Gly
          125               130               135

Glu Ala Lys Thr Ala Val Glu Asn Tyr Leu Ile Gly Ser Pro Val Val
          140               145               150               155

Asp Ser Gln Lys Leu Val Tyr Ser Asp Phe Ser Glu Ala Ala Cys Lys
          160               165               170

Val Asn Asn Ser Asn Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly
          175               180               185

Gly Gly Thr Pro Glu Met Pro Val Leu Glu Asn Arg Ala Ala Gln Gly
          190               195               200

Asp Ile Thr Ala Pro Gly Gly Ala Arg Arg Leu Thr Gly Asp Gln Thr
          205               210               215

Ala Ala Leu Arg Asp Ser Leu Ser Asp Lys Pro Ala Lys Asn Ile Ile
          220               225               230               235

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Leu Leu Ile Gly Asp Gly Met Gly Asp Ser Glu Ile Thr Ala Ala Arg
 240 245 250
 Asn Tyr Ala Glu Gly Ala Gly Gly Phe Phe Lys Gly Ile Asp Ala Leu
 255 260 265
 Pro Leu Thr Gly Gln Tyr Thr His Tyr Ala Leu Asn Lys Lys Thr Gly
 270 275 280
 Lys Pro Asp Tyr Val Thr Asp Ser Ala Ala Ser Ala Thr Ala Trp Ser
 285 290 295
 Thr Gly Val Lys Thr Tyr Asn Gly Ala Leu Gly Val Asp Ile His Glu
 300 305 310 315
 Lys Asp His Pro Thr Ile Leu Glu Met Ala Lys Ala Ala Gly Leu Ala
 320 325 330
 Thr Gly Asn Val Ser Thr Ala Glu Leu Gln Asp Ala Thr Pro Ala Ala
 335 340 345
 Leu Val Ala His Val Thr Ser Arg Lys Cys Tyr Gly Pro Ser Ala Thr
 350 355 360
 Ser Glu Lys Cys Pro Gly Asn Ala Leu Glu Lys Gly Gly Lys Gly Ser
 365 370 375
 Ile Thr Glu Gln Leu Leu Asn Ala Arg Ala Asp Val Thr Leu Gly Gly
 380 385 390 395
 Gly Ala Lys Thr Phe Ala Glu Thr Ala Thr Ala Gly Glu Trp Gln Gly
 400 405 410
 Lys Thr Leu Arg Glu Gln Ala Gln Ala Arg Gly Tyr Gln Leu Val Ser
 415 420 425
 Asp Ala Ala Ser Leu Asn Ser Val Thr Glu Ala Asn Gln Gln Lys Pro
 430 435 440
 Leu Leu Gly Leu Phe Ala Asp Gly Asn Met Pro Val Arg Trp Leu Gly
 445 450 455
 Pro Lys Ala Thr Tyr His Gly Asn Ile Asp Lys Pro Ala Val Thr Cys
 460 465 470 475
 Thr Pro Asn Pro Gln Arg Asn Asp Ser Val Pro Thr Leu Ala Gln Met
 480 485 490
 Thr Asp Lys Ala Ile Glu Leu Leu Ser Lys Asn Glu Lys Gly Phe Phe
 495 500 505
 Leu Gln Val Glu Gly Ala Ser Ile Asp Lys Gln Asp His Ala Ala Asn
 510 515 520
 Pro Cys Gly Gln Ile Gly Glu Thr Val Asp Leu Asp Glu Ala Val Gln
 525 530 535

Arg Ala Leu Glu Phe Ala Lys Lys Glu Gly Asn Thr Leu Val Ile Val
 540 545 - 550 555

Thr Ala Asp His Ala His Ala Ser Gln Ile Val Ala Pro Asp Thr Lys
 560 565 570

Ala Pro Gly Leu Thr Gln Ala Leu Asn Thr Lys Asp Gly Ala Val Met
 575 580 585

Val Met Ser Tyr Gly Asn Ser Glu Glu Asp Ser Gln Glu His Thr Gly
 590 595 600

Ser Gln Leu Arg Ile Ala Ala Tyr Gly Pro His Ala Ala Asn Val Val
 605 610 615

Gly Leu Thr Asp Gln Thr Asp Leu Phe Tyr Thr Met Lys Ala Ala Leu
 620 625 630 635

Gly Leu Lys